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## Restriction Map of the RSV G Gene

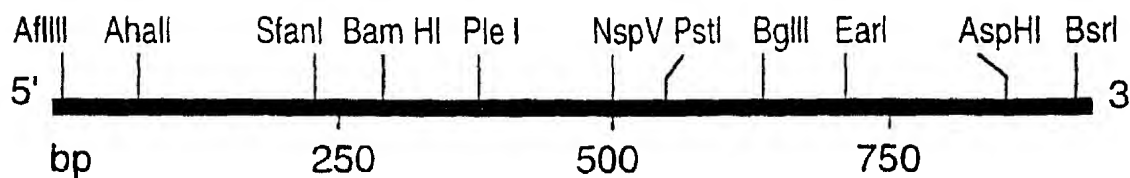


FIG.1



FIG.2A

10	19	28	37	46	55
TGCAAC ATG TOC AAA AAC AAG GAC CAA CGC ACC GCT AAG ACA CTA GAA AAG ACC					
Met Ser Lys Asn Lys Asp Gln Arg Thr Ala Lys Thr Leu Glu Lys Thr					
64	73	82	91	100	109
TGG GAC ACT CTC AAT CAT TTA TTA TTC ATA TCA TCG GGC TTA TAT AAG TTA AAT					
Trp Asp Thr Leu Asn His Leu Leu Phe Ile Ser Ser Gly Leu Tyr Lys Leu Asn					
118	127	136	145	154	163
CTT AAA TCT GTA GCA CAA ATC ACA TTA TOC ATT CTG GCA ATG ATA ATC TCA ACT					
Leu Lys Ser Val Ala Gln Ile Thr Leu Ser Ile Leu Ala Met Ile Ile Ser Thr					
172	181	190	199	208	217
TCA CTT ATA ATT ACA GCC ATC ATA TTC ATA GCC TCG GCA AAC CAC AAA GTC ACA					
Ser Leu Ile Ile Thr Ala Ile Ile Phe Ile Ala Ser Ala Asn His Lys Val Thr					
226	235	244	253	262	271
CTA ACA ACT GCA ATC ATA CAA GAT GCA ACA AGC CAG ATC AAG AAC ACA ACC CCA					
Leu Thr Thr Ala Ile Ile Gln Asp Ala Thr Ser Ser Gln Ile Lys Asn Thr Thr Pro					
280	289	298	307	316	325
ACA TAC CTC ACT CAG GAT OCT CAG CTT GGA ATC AGC TTC TCC AAT CTG TCT GAA					
Thr Tyr Leu Thr Thr Gln Asp Pro Gln Leu Gly Ile Ser Phe Ser Asn Leu Ser Glu					



FIG.2B

334	343	352	361	370	379
ATT ACA TCA CAA ACC ACC ACC ATA GCT TCA ACA ACA CCA GGA GTC AAG TCA					
Ile Thr Ser Gln Thr Thr Thr Thr Thr Thr Thr Thr Thr Thr Thr Thr Thr Thr					
388	397	406	415	424	433
AAC CTG CAA CCC ACA ACA GTC AAG ACT AAA AAC ACA ACA ACC CAA ACA CAA					
Asn Leu Gln Pro Thr Thr Thr Thr Thr Thr Thr Thr Thr Thr Thr Thr Thr Thr					
442	451	460	469	478	487
CCC AGC AAG CCC ACT ACA CAA CAA CAA CAA CCA CCA CCA AAA AAA CCC AAT					
Pro Ser Lys Pro Thr Thr Thr Thr Thr Thr Thr Thr Thr Thr Thr Thr Thr Thr					
496	505	514	523	532	541
AAT GAT TTT CAC TTC GAA GTG TTT AAC TTT GTA CCC TGC AGC ATA TGC AGC AAC					
Asn Asp Phe His Phe Glu Val Phe Asn Phe Val Pro Cys Ser Ile Cys Ser Asn					
550	559	568	577	586	595
AAT CCA ACC TGC TGG GCT ATC TGC AAA AGA ATA CCA AAC AAA CCA CCA GGA AAG					
Asn Pro Thr Cys Trp Ala Ile Cys Lys Arg Ile Pro Asn Lys Lys Pro Gly Lys					
604	613	622	631	640	
AAA ACC ACC AAG OCT ACA AAA CCA ACC TTC AAG ACA ACC AAA GAT AAA GAT					
Lys Thr Thr Thr Lys Pro Thr Thr Lys Lys Pro Thr Thr Thr Thr Thr Thr Thr					

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FIG.2C

658            667            676            685            694            703  
 CTC AAA CCT CAA ACC ACT AAA CCA AAG GAA GTA CCC ACC ACC ACC CCC ACA GAA  
 Leu Lys Pro Gln Thr Thr Lys Pro Lys Glu Val Pro Thr Thr Lys Pro Thr Glu

712            721            730            739            748            757  
 GAG CCA ACC ATC AAC ACC ACC AAA ACA AAC ATC ACA ACT ACA CTG CTC ACC AAC  
 Glu Pro Thr Ile Asn Thr Thr Lys Thr Asn Ile Thr Thr Leu Leu Thr Asn

766            775            784            793            802            811  
 AAC ACC ACA CGA AAT CCA AAA CTC ACA AGT CAA ATG GAA ACC TTC CAC TCA ACC  
 Asn Thr Thr Gly Asn Pro Lys Leu Thr Ser Gln Met Glu Thr Phe His Ser Thr

820            829            838            847            856            865  
 TCC TCC GAA GGC AAT CTA AGC OCT TCT CAA GTC TCC ACA ACA TOC GAG CAC CCA  
 Ser Ser Glu Gly Asn Leu Ser Pro Ser Gln Val Ser Thr Thr Ser Glu His Pro

874            883            892            901            914  
 TCA CAA CCC TCA TCT CCA CCC AAC ACA ACA CGC CAG TAGTTATTAA AAAAAAAA  
 Ser Gln Pro Ser Ser Pro Pro Asn Thr Thr Arg Gln .

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FIG.3A

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CAC AAA GTC ACA CTA ACA ACT GCA ATC ATA CAA GAT GCA ACA AGC CAG ATC AAG	54
His Lys Val Thr Leu Thr Thr Ala Ile Ile Gln Asp Ala Thr Ser Gln Ile Lys	18
AAC ACA ACC CCA ACA TAC CTC ACT CAG GAT CCT CAG CTT GGA ATC AGC TTC TTC	108
Asn Thr Thr Pro Thr Tyr Thr Leu Thr Thr Gln Asp Pro Gln Leu Gly Ile Ser Phe Ser	36
AAT CTG TCT GAA ATT ACA TCA CAA ACC ACC ATA GCT CTA GCT TCA ACA ACA CCA	162
Asn Leu Ser Glu Ile Thr Ser Gln Thr Thr Thr Ile Leu Ala Ser Thr Thr Pro	54
GGG GTC AAG TCA AAC CTG CAA CCC ACA ACA GTC AAG ACT AAA AAC ACA ACA ACA	216
Gly Val Lys Ser Asn Leu Gln Pro Thr Thr Thr Val Lys Thr Lys Asn Thr Thr Thr	72
ACC CAA ACA CCA CCC AGC AAG CCC ACT ACA AAA CAA CCC CAA AAC AAA CCA CCA	270
Thr Gln Thr Thr Gln Pro Ser Lys Pro Thr Thr Thr Lys Gln Arg Gln Asn Lys Pro Pro	90
AAC AAA CCC AAT AAT GAT TTT CAC TTC GAA GIG TTT AAC TTT GTA CCC TGC AGC	324
Asn Lys Pro Asn Asn Asp Phe His Phe Glu Val Phe Asn Phe Val Pro Cys Ser	108
ATA TGC AGC AAC AAT CCA ACC TGC TGG GCT ATC TCC AAA AGA ATA CCA AAC AAA	378
Ile Cys Ser Asn Asn Pro Thr Cys Thr Ala Ile Cys Lys Arg Ile Pro Asn Lys	126
AAA CCA GGA AAG AAA ACC ACC ACC AAG CCT ACA AAA AAA CCA ACC TTC AAG ACA	432
Lys Pro Gly Lys Lys Thr Thr Thr Lys Pro Thr Lys Lys Pro Thr Phe Lys Thr	144

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## FIG.3B

ACC AAA AAA GAT CTC AAA OCT CAA ACC ACT AAA CCA AAG GAA GTA CCC ACC ACC 486  
 Thr Lys Lys Asp Leu Lys Pro Gln Thr Thr Lys Pro Lys Glu Val Pro Thr Thr 162  
  
 AAG CCC ACA GAA GAG CCA ACC ATC AAC ACC ACC AAA ACA AAC ATC ACA ACT ACA 540  
 Lys Pro Thr Glu Glu Pro Thr Thr Ile Asn Thr Thr Lys Thr Asn Ile Thr Thr 180  
  
 CTG CTC ACC AAC AAC ACC ACA CGA AAT CCA AAA CTC ACA AGT CAA ATG GAA ACC 594  
 Leu Leu Thr Asn Asn Thr Thr Gly Asn Pro Lys Leu Thr Ser Gln Met Glu Thr 198  
  
 TTC CAC TCA ACC TCC TCC GAA CGC AAT CTA AGC OCT TCT CAA GTC TCC ACA ACA 648  
 Phe His Ser Thr Ser Ser Glu Glu Asn Leu Ser Pro Ser Gln Val Ser Thr Thr 216  
  
 TCC GAG CAC CCA TCA CAA CCC TCA TCT CCA CCC AAC ACA ACA CGC CAG TAG 699  
 Ser Glu His Pro Ser Gln Pro Ser Ser Pro Pro Asn Thr Thr Arg Gln 232  
  
 TTATTTAA AAAAAAAAAA

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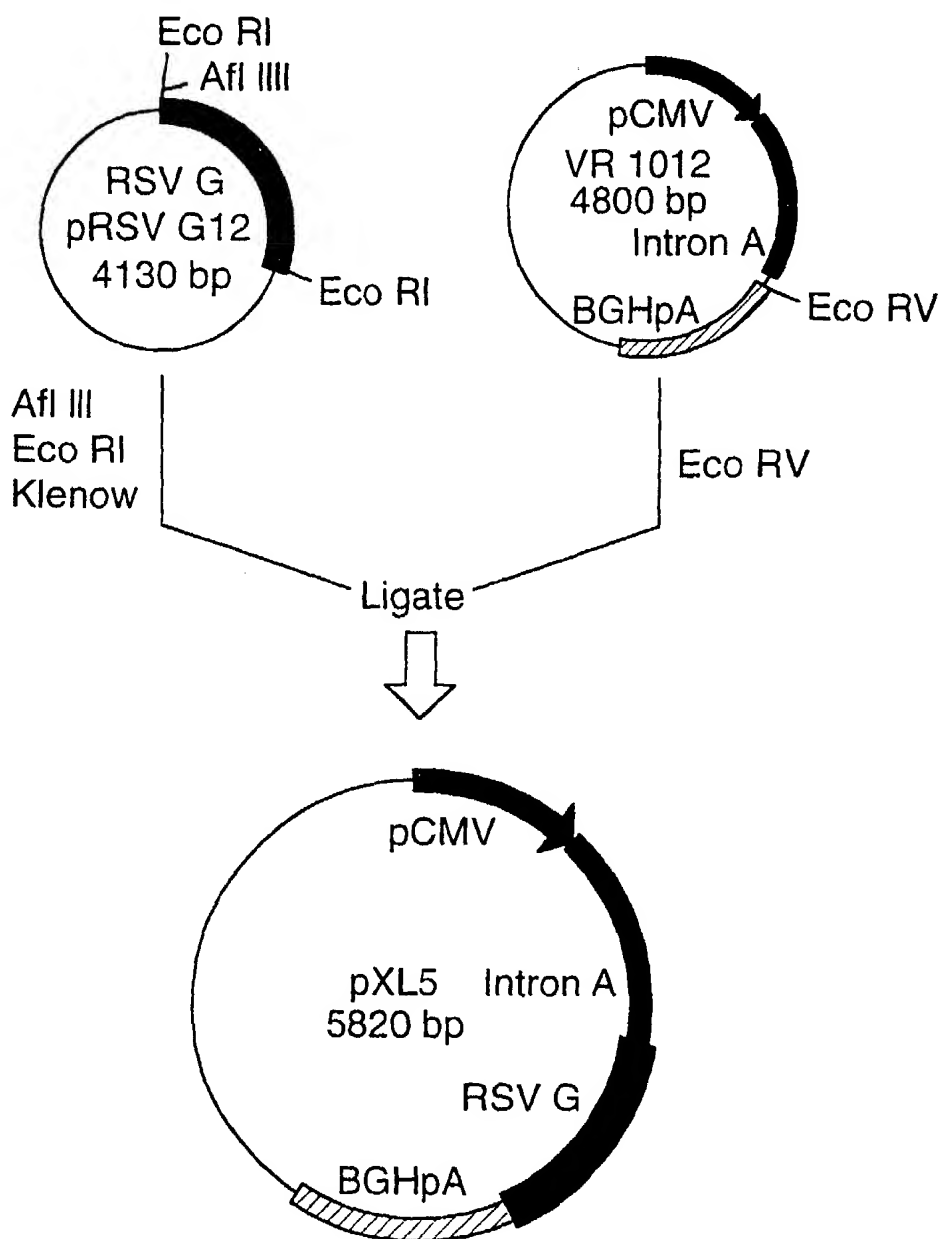


FIG.4.

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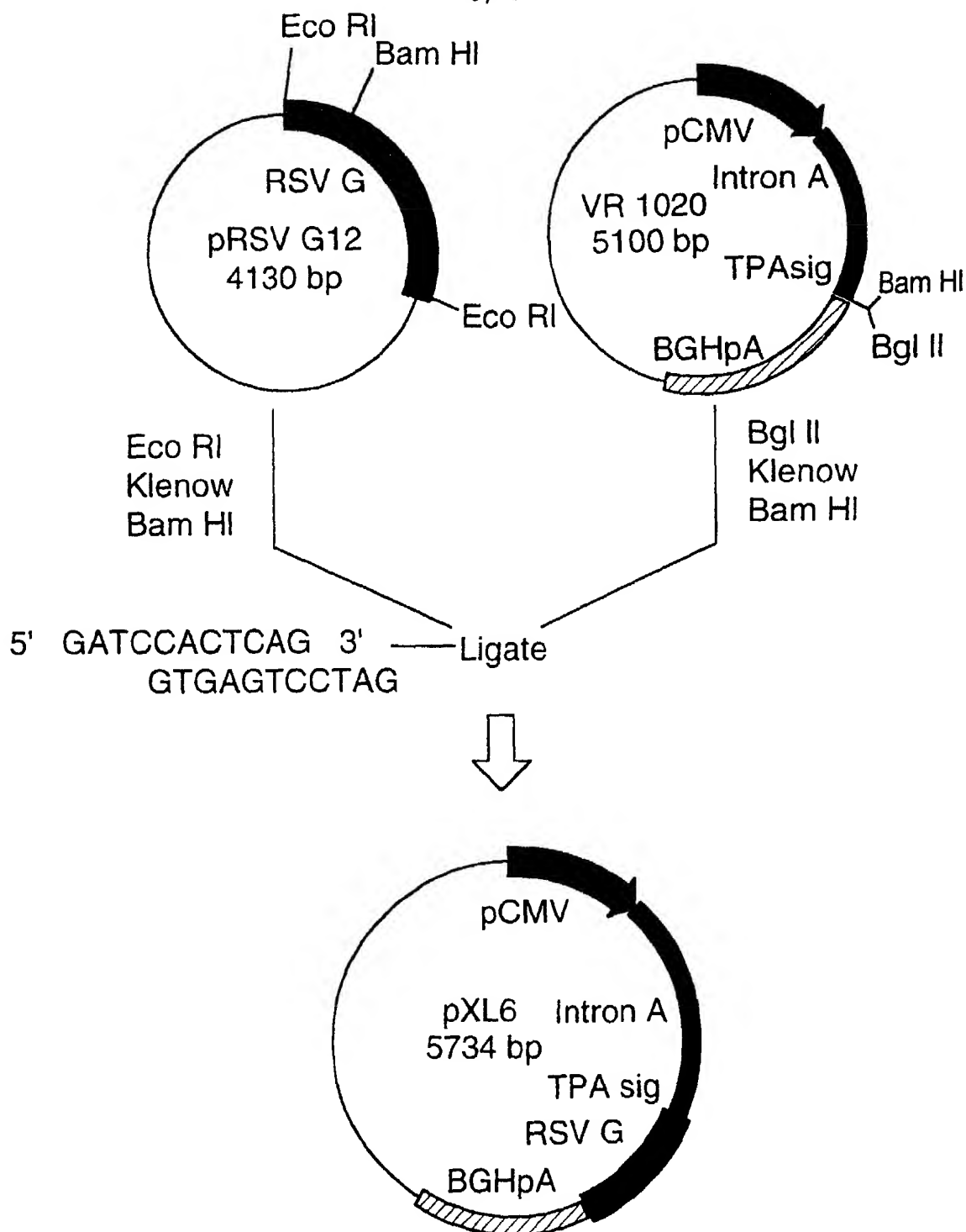


FIG.5

FIG.6A

10 20 30 40 50 60 70  
 TOGGCGGTTT CCGGATGAC GGTCAGAAC TCCTGACACAT GCAGCTCCCG GAGACGGTCA CAGCTTGCT  
 80 90 100 110 120 130 140  
 GTAAAGCGGAT GCGGGAGCA GACAAGCCCG TCAGCGGGTG TCAGCGGGTG TGGCGGGTG TGGCGGCTG  
 150 160 170 180 190 200 210  
 CTTAACATAG CCGCATCAGA GCAGATTGTA CTGAGAGTGC ACCATATCCG GIGTGAATA CCGCACAGAT  
 220 230 240 250 260 270 280  
 GGGTAAGGAG AAAATACCG ATCAGATTGG CTATTGGCA TTGCATACGT TGTATOCATA TCATAATATG  
 290 300 310 320 330 340 350  
 TACATTATTA TGGCCATG TCCAAACATTA CCGCCATGTT GACATTGATT ATTIGACTAGT TATTAAATAGT  
 360 370 380 390 400 410 420  
 AATCAATTAC GGGGICATTA GTTCATAGC CATATATGGA GTTCCCGGTT ACATAACTTA CCGPAAATGG  
 430 440 450 460 470 480 490  
 CCGGCTGGC TCACGGGCA ACCAGCCCGG CCGATTGACG TCAATAATGA CCGTATGTTCC CATAGTAAAG  
 500 510 520 530 540 550 560  
 CCAATAGGA CTTTCCATTG ACGTCAATGG GGGAGTATT TACGGTAAAC TGGCCACTTG GCAGTACATC

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FIG.6B

570 580 590 600 610 620 630  
 AAGIGTATCA TATGCCAAGT ACGCCCCCTA TTGACGTCAA TCACGGTAAA TGGCCCCGCTT GGCATTATGC  
  
 640 650 660 670 680 690 700  
 CCAGTACATG ACCTTATGGG ACITTTCTAC TTGGCAGTAC ATCTACGTAT TAGTCATCGC TATTACCATG  
  
 710 720 730 740 750 760 770  
 GTGATGGGGT TTTCGCAGTA CATCAATGGG CGTCGATAGC GGTTCAGTC ACGGGGATTT CCAAGICTOC  
  
 780 790 800 810 820 830 840  
 ACCCCATTGA CGTCAATGGG AGTTTGTGTTT GGCACCAAAA TCAACGGGAC TTTCACAAAAT GTCGTAAACAA  
  
 850 860 870 880 890 900 910  
 CTCGCCCCCA TTGACGGCAA TGGGCGGTAG GGGTGTACGG TGGGAGGICT ATATAAGCAG AGCTCGTTTA  
  
 920 930 940 950 960 970 980  
 GTGAACCGTC AGATGGCCTG GAGACGGCAT CCACGCTGTT TTGACCTCCA TAGAAGACAC CCGGACCGAT  
  
 990 1000 1010 1020 1030 1040 1050  
 CCAGCCTCG CGGCGCGGAA CCGTGCATTG GAACGGGAT TCCCCGIGCC AAGAGTACG TAAGTACCGC  
  
 1060 1070 1080 1090 1100 1110 1120  
 CTATAGACTC TATAGGCACA CCCCCTTGGC TCTTATGCAT GCTATACIGT TTTTGGCTTG GGGCCATAC

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FIG.6C

1130 1140 1150 1160 1170 1180 1190  
 ACCCGGCTT CCTTATGCTA TAGGICATGG TATACCTTAG CCTATAGGCG TGGGTTATTC ACCATTATTC  
 1200 1210 1220 1230 1240 1250 1260  
 ACCACTCCCC TATTGGTGAC GATACCTTTC ATTACTAATC CATAACATGG CTCTTTGGCA CAACTATCTC  
 1270 1280 1290 1300 1310 1320 1330  
 TATTGGCTAT ATGCCAATAC TCTGTCCTTC ACAGACIGAC ACGGACCTCG TATTTTTCAC GGATGGGGC  
 1340 1350 1360 1370 1380 1390 1400  
 CCATTATTA TTTACAAATT CACATATACA ACAACGCCGT CCCCCGIGCC GCGAGTTTTT ATTAAACATA  
 1410 1420 1430 1440 1450 1460 1470  
 GCGTGGATC TOCAGCGAA TCTCGGGTAC GGTGTCCTCT CATGGGCTCT TCTCCGGTAG CGCGGGAGCT  
 1480 1490 1500 1510 1520 1530 1540  
 TOCACATCCG AGCCCTGGTC CCATGCTCC AGCGGCTCAT GGTCGCTCGG CAGCTCCTTG CTCCTAACAG  
 1550 1560 1570 1580 1590 1600 1610  
 TCGAGGCCAG ACTTAGGCAC AGCACAAATC CCACCAACAC CAGGTGTCGG CACAAGGCCG TGGCGGTAGG  
 1620 1630 1640 1650 1660 1670 1680  
 GTATGTGCT GAAATGAGC GTGGAGATTC GGTTCGACG GCTGACCGAG ATGGAAGACT TAAGCCAGCG

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FIG.6D

1690	1700	1710	1720	1730	1740	1750
GCAGAAGAAG	ATGCAGGCAG	CTGAGTGTGT	GTATTCTCAT	AAGAGTCAGA	GGTAACCTCC	GTTCGGGTGC
1760	1770	1780	1790	1800	1810	1820
TGTTAACGGT	GGAGGGCAGT	GTAGTCTGAG	CAGTACTCGT	TGCTGCGCGG	CGCGCCACCA	GACATAATAG
1830	1840	1850	1860	1870	1880	1890
CTGACAGACT	AACAGACTGT	TOCTTTCCAT	GGGCTTTTC	TGCAGTCACC	GTGTCGACA	CGTGTGATCA
1900	1910	1920	1930	1940	1950	1960
GATAATGCGG	CCGCTCTAGA	CCAGGGCCCT	GGATCCAGAT	CCTCCTGCGC	TCTAGTTC	CAGCCATCTG
1970	1980	1990	2000	2010	2020	2030
TTGTTTGCCC	CICCCCCGIG	CCTTCTCTCA	CCCTGGAAG	TGCCACTCCC	ACTGTCTTT	CTTAATAAAA
2040	2050	2060	2070	2080	2090	2100
TCAGGAAATT	GCATCGCATT	GCTGAGTAG	GTGTCATTCT	ATTCTGCGCG	GTCGGGTGG	GCAGGACAGC
2110	2120	2130	2140	2150	2160	2170
AAGCGGAGG	ATTGGGAAGA	CAATAGCAGG	CATGCTGGCG	ATGCGGTGGG	CTCTATGGGT	ACCCAGGTGC
2180	2190	2200	2210	2220	2230	2240
TGAGCAATTG	ACCCGGTTCC	TGCTGGGCCA	GAAAGAAGCA	GGCACATCCC	CTTCTCTGIG	ACACACCCCTG

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FIG.6E

2250 2260 2270 2280 2290 2300 2310  
 TCCAGCCCC TGGTCTTAG TTCCAGCCCC ACTCATAGGA CACTCATAGC TCAGGAGGGC TCCGCCCTTCA  
  
 2320 2330 2340 2350 2360 2370 2380  
 ATCCACCCCG CTAAAGTACT TGGAGGGGTC TCTCCCTCC TCATCAGCCC ACCAAACCAA ACCTAGCCTC  
  
 2390 2400 2410 2420 2430 2440 2450  
 CAAGAGTCGG AAGAAATTAA ACCAAGATAG GCTATTAAAT GCAGAGGGAG AGAAAAATGCC TCCAAACATGT  
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 2460 2470 2480 2490 2500 2510 2520  
 GAGCAAGTAA TCAGAGAAAT CATAGAAATT CTTCGGCTTC CTGGCTACT GACTGGCTCC GCTGGGTGT  
  
 2530 2540 2550 2560 2570 2580 2590  
 TCGGCTGGCG CGAGCGGTAT CAGCTCAGTC AAAGCGGTA ATACGGTTAT CCACAGATC AGGGGATAAC  
  
 2600 2610 2620 2630 2640 2650 2660  
 GCAGGAAAGA ACATGTGAGC AAAAGGCCAG CAAAGGCCA GGAACCGTAA AAAGCGCGG TTGCTGGCGT  
  
 2670 2680 2690 2700 2710 2720 2730  
 TTTTCCATAG GCTCCGCCCC CCCTGAGGAG ATCACAAAAA TCGACCTCA AGTCAGAGGT GCGGAAACCC  
  
 2740 2750 2760 2770 2780 2790 2800  
 GACAGGACTA TAAAGATACC AGGGTTTCC CCCTGGAAGC TCCCTGGTGC GCCTCTCTGT TCCGACCTTG

FIG.6F

2810 2820 2830 2840 2850 2860 2870  
 CCGCTTACCG GATACCTGTC CGCCTTTCTC CCTTCGGGAA GGGGGGGCT TTCTCATAGC TCAAGCTGTA  
  
 2880 2890 2900 2910 2920 2930 2940  
 GGTATCTCAG TTCCGGGTAG GTCGTTGCT CCAAGCTGGG CTGCTGTCAC GAAACCCCGG TTCAGCCCGA  
  
 2950 2960 2970 2980 2990 3000 3010  
 CCGCTGGCC TTATCCGGTA ACTATCGTCT TCAGTCCAC CCGTAAGAC ACGACTTATC GCCACTGGCA  
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 3020 3030 3040 3050 3060 3070 3080  
 GCAGCCACTG GTAACACAGAT TAGCAGAGCG AGGTATGTAG GCGTCTTAC ACAGTCTCTG AAGTGCTGC  
  
 3090 3100 3110 3120 3130 3140 3150  
 CTAACTACCG CTACACTAGA AGAACAGTAT TTGGTATCTG CGCTCTGCTG AAGCCAGTGA CCTTCGGAAA  
  
 3160 3170 3180 3190 3200 3210 3220  
 AAGAGTTGGT AGCTCTTGAT CCGGCAACA AACCAACGCT GGTAAGCGTG GTTTTTTTGT TTGCAAGCAG  
  
 3230 3240 3250 3260 3270 3280 3290  
 CAGATTACCG GCAGAAAAA AGGATCTCAA GAAGATCTT TCACTTTTC TACGGGGTCT GAACCTCAGT  
  
 3300 3310 3320 3330 3340 3350 3360  
 GGAACGAAA CIGACGTAA GGGATTTGG TCATGAGAT ATCAAAAAGG ATCTTCACCT AGATCCCTTT

FIG.6G

3370	3380	3390	3400	3410	3420	3430
AAATTAAAA	TGAAGTTT	AATCAATCTA	AAGTATATAT	GAGTAAACTT	GGTCTGACAG	TTACCAATGC
3440	3450	3460	3470	3480	3490	3500
TTAATCAGIG	AGGCACCTAT	CTCAGCGATC	TGCTATTTC	GTTCATCCAT	AGTTGCCCTG	CTCGGGGGGG
3510	3520	3530	3540	3550	3560	3570
GGGGGGGCTG	AGGCTGCTCT	CGTGAAGAAG	GTGTTGCTGA	CTCATACCAG	GGCTGAATCG	CCCCATCATC
3580	3590	3600	3610	3620	3630	3640
CAGCCAGAAA	GTCAGGGAGC	CACGGTTGAT	GAGAGCTTTG	TTGTAGGTGG	ACCAGTTGGT	GATTTTGAAC
3650	3660	3670	3680	3690	3700	3710
TTTTCCTTTG	CCACGGAACG	GTCCTGGTTG	TCGGGAAGAT	GGGTGATCTG	ATCTTTCAC	TCAGCAAAAG
3720	3730	3740	3750	3760	3770	3780
TTTCATTTAT	TCAACAAAGC	CGCGTCCCG	TCAAGTCAGC	GTAATGCTCT	GCCAGTGITA	CAACCAATTA
3790	3800	3810	3820	3830	3840	3850
ACCAATTGIG	ATTAGAAAAA	CTCATCGAGC	ATCAAATGAA	ACTGCAATTT	ATTGATATCA	GGATTATCAA
3860	3870	3880	3890	3900	3910	3920
TACCATATTT	TTGAAAAAGC	CGTTTCTGTA	ATGAGGAGAG	AAACTCACCG	AGGCAGTTC	ATAGGATGCC

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FIG.6H

3930 3940 3950 3960 3970 3980 3990  
 AATATCTCTGG TATCGGCTCTG CGATTCTCGAC TCGICCAACA TCAATACAC CTATTATATT CCGCTCGICA  
  
 4000 4010 4020 4030 4040 4050 4060  
 AAAATAAGGT TATCAAGTGA GAAATCACCA TGAGTGACGA CTGAATCCGG TGAGAAATGG AAAAGCTTAT  
  
 4070 4080 4090 4100 4110 4120 4130  
 GCATTTCCTTT CCAGACTTGT TCAACAGGCC AGCCATTAG CTGCTGATCA AAATCACCTCG CATCAACCAA  
  
 4140 4150 4160 4170 4180 4190 4200  
 ACCGTTATTC ATTCTGTGATT GCGCCCTGAGC GAGACGAAAT ACGCGATCGC TGTATAAAGG ACAATTACAA  
  
 4210 4220 4230 4240 4250 4260 4270  
 ACAGGAATCG AATGCAACCG GCGCCAGGAAC ACTGCCAGCG CATCAACAAT ATTTTCACTT GAATCAGGAT  
  
 4280 4290 4300 4310 4320 4330 4340  
 ATTCTTCTAA TACCTGGAAT GCCTGTTTTC CCGCGATCGC AGTGGTGAGT AACCATGCTAT CATCAGGAGT  
  
 4350 4360 4370 4380 4390 4400 4410  
 ACGGATAAAA TGCCTTGATGG TCGGAAGAGG CATAAATTC GTACGCCAGT TTAGTCTGAC CATCTCATCT  
  
 4420 4430 4440 4450 4460 4470 4480  
 GTAAATCAT TGGCAACGCT ACCCTTGGCA TGTCTTCAGAA ACAACTCTGG CGCATCGGGC TTCCCATACA

FIG.6I

4490 4500 4510 4520 4530 4540 4550  
 ATCGATAGAT TGTCGCACCT GATTCGCGCA CATTATCGCG AGCCCATTTA TACCCATATA AATCAGCATC  
  
 4560 4570 4580 4590 4600 4610 4620  
 CATGTTGGAA TTTAATCGCG GCGTCGAGCA AGACGTTTCC CGTTGAATAT GGCICATAAC GTTCTTGTGA  
  
 4630 4640 4650 4660 4670 4680 4690  
 TTACIGTTTA TGTAAGCAGA CAGTTTATT GTTCATGATG ATATATTTTT ATCTTGTGCA ATGTAACATC  
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 4700 4710 4720 4730 4740 4750 4760  
 AGAGATTTTG AGACACAAGG TGGCTTTCC CCCCCCCCCA TTATTTGAAGC ATTATCAGG GTTATTGTCT  
  
 4770 4780 4790 4800 4810 4820 4830  
 CATCAGCGCA TACATATTTG AATGTATTTA GAAAAATAAA CAAATAGCGG TTCCGGCCAC ATTTCGCCGA  
  
 4840 4850 4860 4870 4880 4890 4900  
 AAAGTCCAC CTGACGCTA AGAAACCAT ATTATCATGA CATTAACCTA TAAAAATAGG CGTATCAGCA  
  
 4910  
 GGGCCTTTCG TC

FIG. 7

10	20	30	40	50	60	70
CTGCAGTCAC	CGTGTGTGAC	CAGAGCTGAG	ATCCTACAGG	AGTCCAGGGC	TGGAGAGAAA	ACCTCTGCGA
80	90	100	110	120	130	140
GGAAAGGGAA	GGAGCAAGOC	GTGAATTTAA	GGGACGCTGT	GAAAGCAATCA	TGGATCCCAT	GAAGAGAGGG
150	160	170	180			
CTCTGCTGTG	TGCTGCTGCT	GTGTGGAGCA	GTCTTGTGTT	GGCCCCAGC		

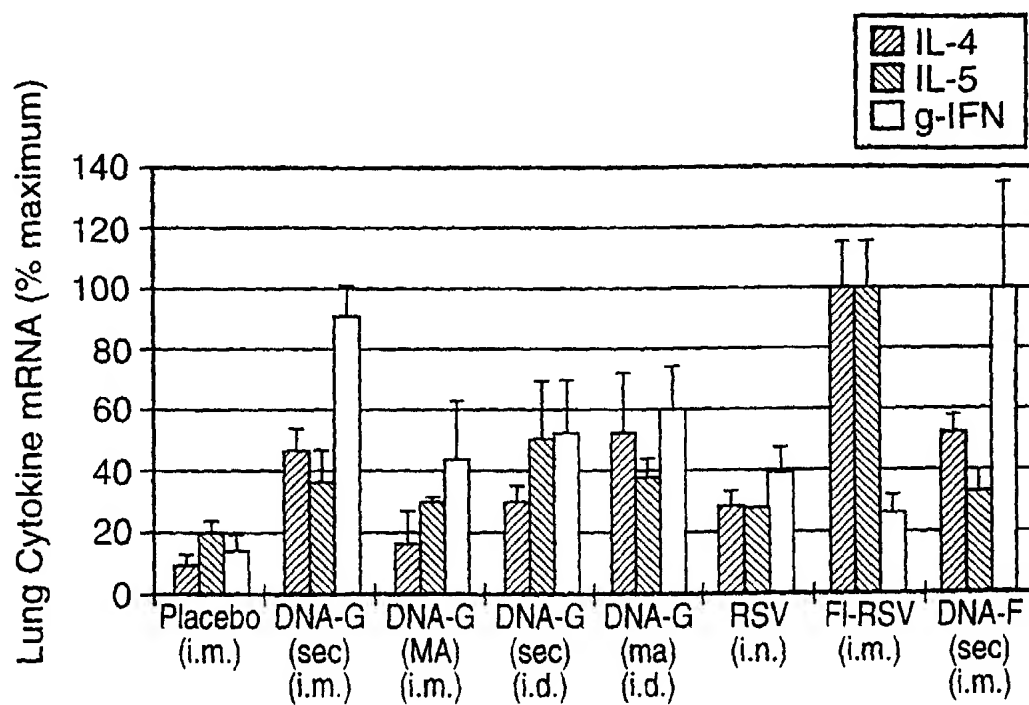


FIG.8